



Docket No.: 466992000221  
(PATENT)

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Patent Application of:  
Chong-Sheng YUAN

Application No.: 10/043,787

Confirmation No.: 9117

Filed: January 10, 2002

Art Unit: 1652

For: METHODS AND COMPOSITIONS FOR  
ASSAYING HOMOCYSTEINE

Examiner: I. Chowdhury

**DECLARATION OF CHONG-SHENG YUAN**

MS Amendment  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Dear Sir:

I, Chong-Sheng Yuan, declare as follows:

1. I am the inventor of the subject matter specifically claimed in the above-referenced patent application U.S. Ser. No. 10/043,787, and I am familiar with the contents thereof.

2. Enclosed herewith are the following exhibits:

Exhibit A. GenBank sequence listing and revision history for L32836;

Exhibit B. GenBank sequence listing and revision history for M15185;

Exhibit C. GenBank sequence listing and revision history for M61831; and

Exhibit D. GenBank sequence listing and revision history for M61832.

3. Based on the information from [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov), the GenBank entry for L32836 was last modified on July 25, 1995 (*See Exhibit A*); the GenBank entry for M15185 was last modified on October 4, 1994 (*See Exhibit B*); the GenBank entry for M61831 was last modified

on November 1, 1994 (See Exhibit C); and the GenBank entry for M61832 was last modified on November 1, 1994 (See Exhibit D). The sequences recited in GenBank entries downloaded at the time as indicated in the references submitted herein as Exhibits A-D are the same as the sequences recited in GenBank entries at the priority date (July 6, 1999) of the present application. Thus, the amendatory material of the Amendment submitted herewith consists of the same material incorporated by reference in the present application. No new matter has been added.

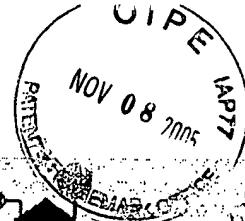
I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

11/07/05

Date

Chong-Sheng Yuan

Chong-Sheng Yuan



PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from  to   Reverse complemented strand Features:  SNP  CDD

1: L32836. Reports Mus musculus (clo...[gi:904131] Links

LOCUS MUSSAH

DEFINITION Mus musculus (clone C7/B9) S-adenosyl homocysteine hydrolase (ahcy) mRNA, complete cds.

ACCESSION L32836

VERSION L32836.1 GI:904131

KEYWORDS S-adenosyl-L-homocysteine hydrolase; adenosylhomocysteinase; copper-binding protein; homocysteine hydrolysis.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2057)

AUTHORS Petrovic, N., Zhou, X.-B., Bethin, K.E., Cimato, T. and Ettinger, M.J.

TITLE Cloning a cDNA for copper binding protein and its identification as S-Adenosyl Homocysteine Hydrolase

JOURNAL Proc. Natl. Acad. Sci. U.S.A. (1994) In press

COMMENT On Jul 25, 1995 this sequence version replaced gi:825467. Original source text: Mus musculus (strain BALB/c, sub\_species domesticus) (clone library: ML1035b phage library (Clontech)) male adult liver cDNA to mRNA.

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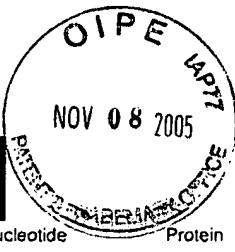
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PubMed Nucleotide Protein

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Structure

PMC

Taxonomy

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## Revision history for L32836

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LocusLink

Clusters of orthologous groups

Protein reviews on the web

| GI     | Version | Update Date          | Status | I                                | II                               |
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| 825467 | 0       | May 23 1995 2:02 PM  | Dead   | <input type="radio"/>            | <input checked="" type="radio"/> |
| 529443 | 0       | Oct 4 1994 3:45 AM   | Dead   | <input type="radio"/>            | <input checked="" type="radio"/> |
| 529443 | 0       | Aug 13 1994 12:21 AM | Dead   | <input type="radio"/>            | <input checked="" type="radio"/> |

Accession L32836 was first seen at NCBI on Aug 13 1994 12:21 AM

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Range: from  to   Reverse complemented strand Features:  SNP  CDD

1: M15185. Reports Rat S-adenosyl-L-... [gi:202803] [Links](#)

**LOCUS** RATAHHA 2029 bp mRNA linear ROD 27-APR-1993  
**DEFINITION** Rat S-adenosyl-L-homocysteine hydrolase mRNA, complete cds.  
**ACCESSION** M15185  
**VERSION** M15185.1 GI:202803  
**KEYWORDS** adenosylhomocysteinase; hydrolase.  
**SOURCE** Rattus sp.  
**ORGANISM** Rattus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
**REFERENCE** 1 (bases 1 to 2029)  
**AUTHORS** Aksamit, R.R.  
**JOURNAL** Unpublished (1987)  
**REFERENCE** 2 (bases 1 to 2029)  
**AUTHORS** Ogawa, H., Gomi, T., Mueckler, M.M., Fujioka, M., Backlund, P.S. Jr.,  
 Aksamit, R.R., Unson, C.G. and Cantoni, G.L.  
**TITLE** Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from rat  
 liver as derived from the cDNA sequence  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 84 (3), 719-723 (1987)  
**PUBMED** 3027698  
**COMMENT** Original source text: Rat liver, cDNA to mRNA.  
 Draft entry and computer-readable sequence for [2], [1] kindly  
 provided by R.R. Aksamit 25-JUL-1988.  
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//

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Oct 4 2005 13:52:42



## Sequence Revision History

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| GI     | Version | Update Date         | Status | I                                | II                               |
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| 202803 | 1       | Oct 4 1994 4:30 AM  | Live   | <input checked="" type="radio"/> | <input checked="" type="radio"/> |
| 202803 | 1       | Apr 27 1993 8:13 PM | Dead   | <input checked="" type="radio"/> | <input checked="" type="radio"/> |

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from  to   Reverse complemented strand Features:  SNP  CDD

1: M61831. Reports Human S-adenosylh...[gi:178276]

LOCUS HUMAHCY 2211 bp mRNA linear PRI 30-OCT-1994  
 DEFINITION Human S-adenosylhomocysteine hydrolase (AHCY) mRNA, complete cds.  
 ACCESSION M61831  
 VERSION M61831.1 GI:178276  
 KEYWORDS S-adenosylhomocysteine hydrolase.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2211)  
 AUTHORS Coulter-Karis, D.E. and Hershfield, M.S.  
 TITLE Sequence of full length cDNA for human S-adenosylhomocysteine hydrolase  
 JOURNAL Ann. Hum. Genet. 53 (Pt 2), 169-175 (1989)  
 PUBMED 2596825  
 COMMENT Original source text: Homo sapiens RNA.  
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11

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| 178276 | 1       | Oct 28 1994 12:49 AM | Dead   | <input checked="" type="radio"/> | <input checked="" type="radio"/> |
| 178276 | 1       | Oct 3 1994 1:52 PM   | Dead   | <input checked="" type="radio"/> | <input checked="" type="radio"/> |
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Range: from  to   Reverse complemented strand Features:  SNP  CDD

1: M61832. Reports Human S-adenosylh...[gi:178278]

LOCUS HUMAHCY2 2084 bp mRNA linear PRI 30-OCT-1994

DEFINITION Human S-adenosylhomocysteine hydrolase (AHCY) mRNA, complete cds.

ACCESSION M61832

VERSION M61832.1 GI:178278

KEYWORDS S-adenosylhomocysteine hydrolase.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2084)

AUTHORS Coulter-Karis, D.E. and Hershfield, M.S.

TITLE Sequence of full length cDNA for human S-adenosylhomocysteine hydrolase

JOURNAL Ann. Hum. Genet. 53 (Pt 2), 169-175 (1989)

PUBMED 2596825

COMMENT Original source text: Homo sapiens RNA.  
From EMBL entry HSAHCY2; dated 29-MAR-1991.

FEATURES Location/Qualifiers

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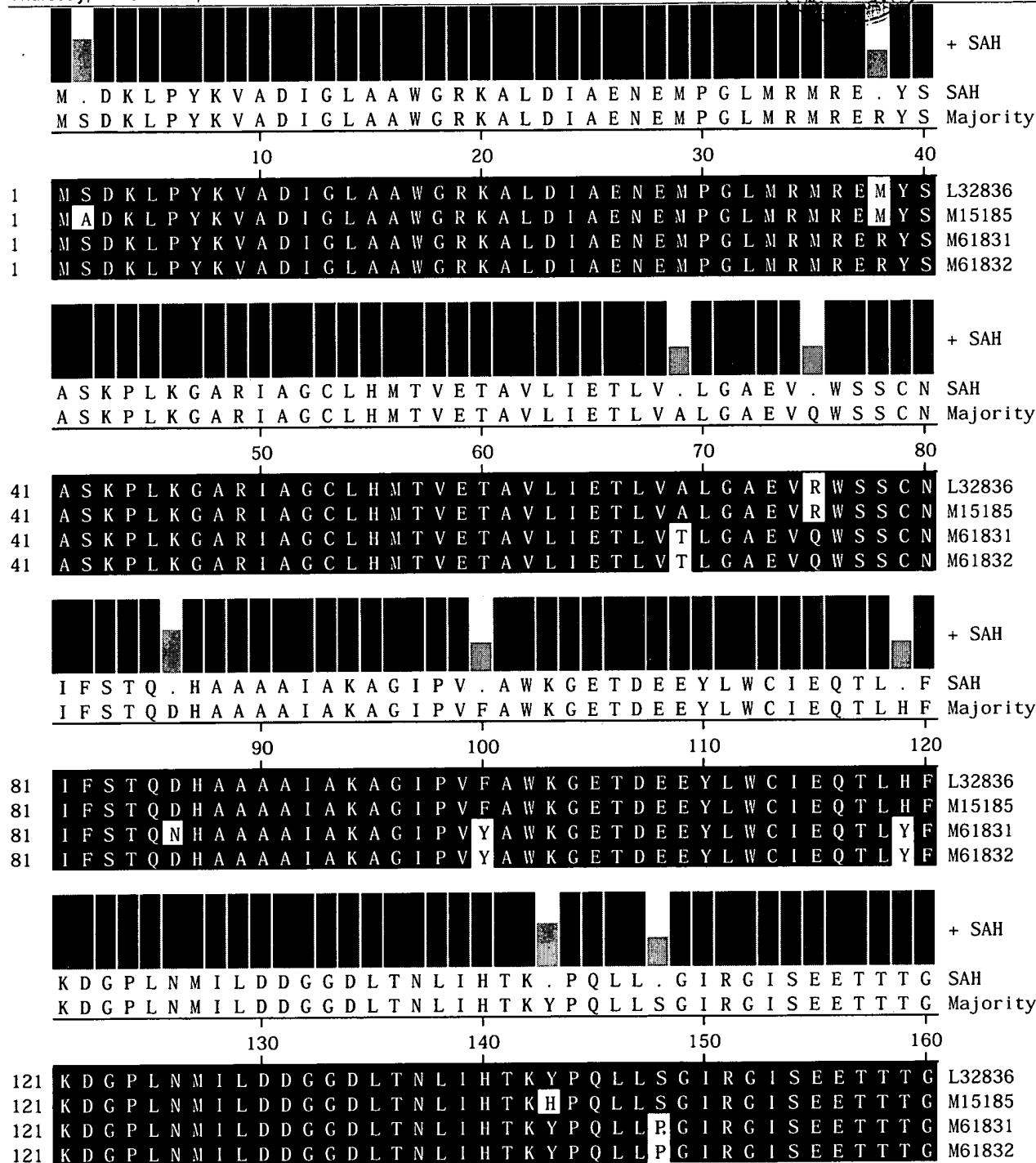
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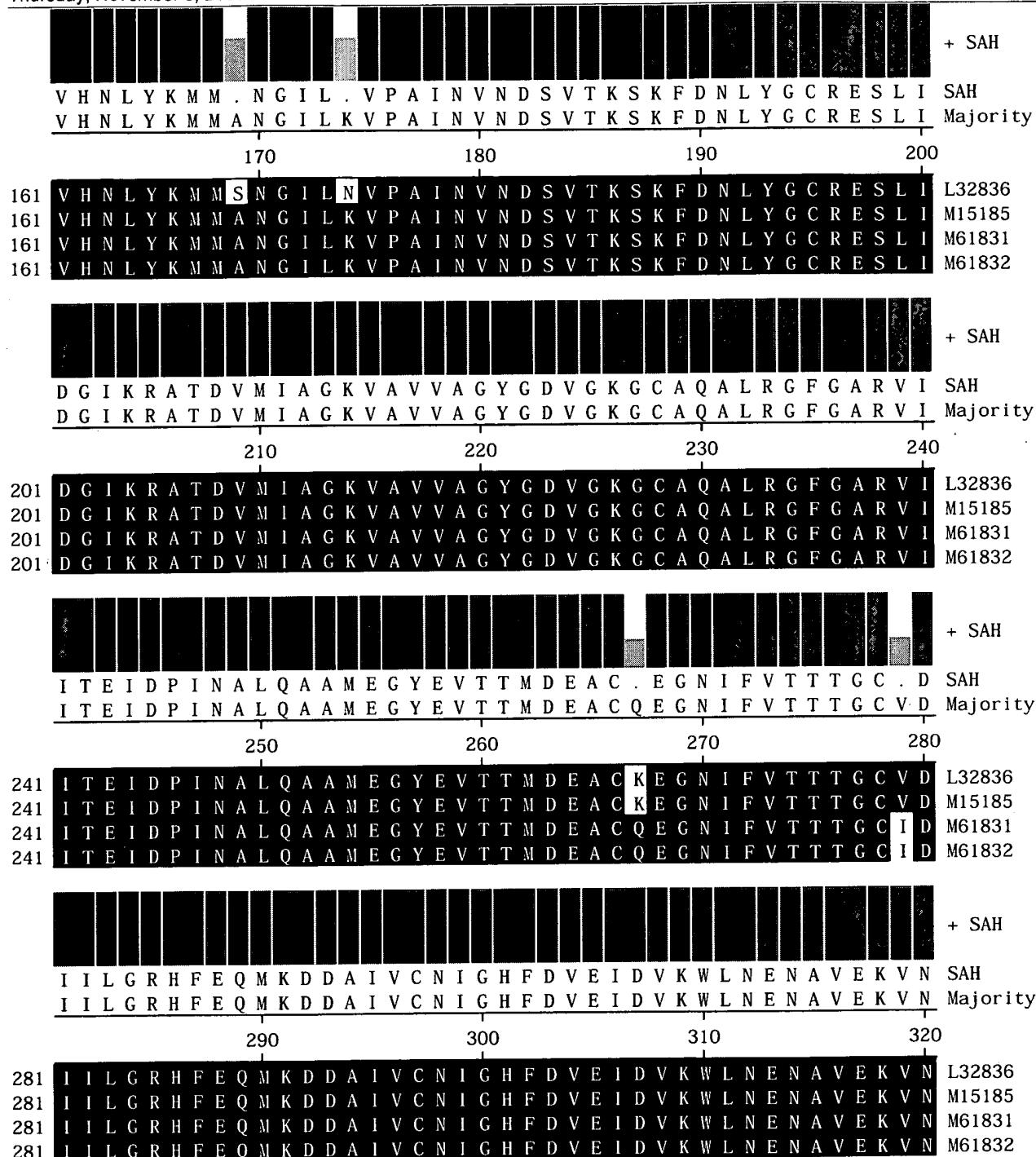
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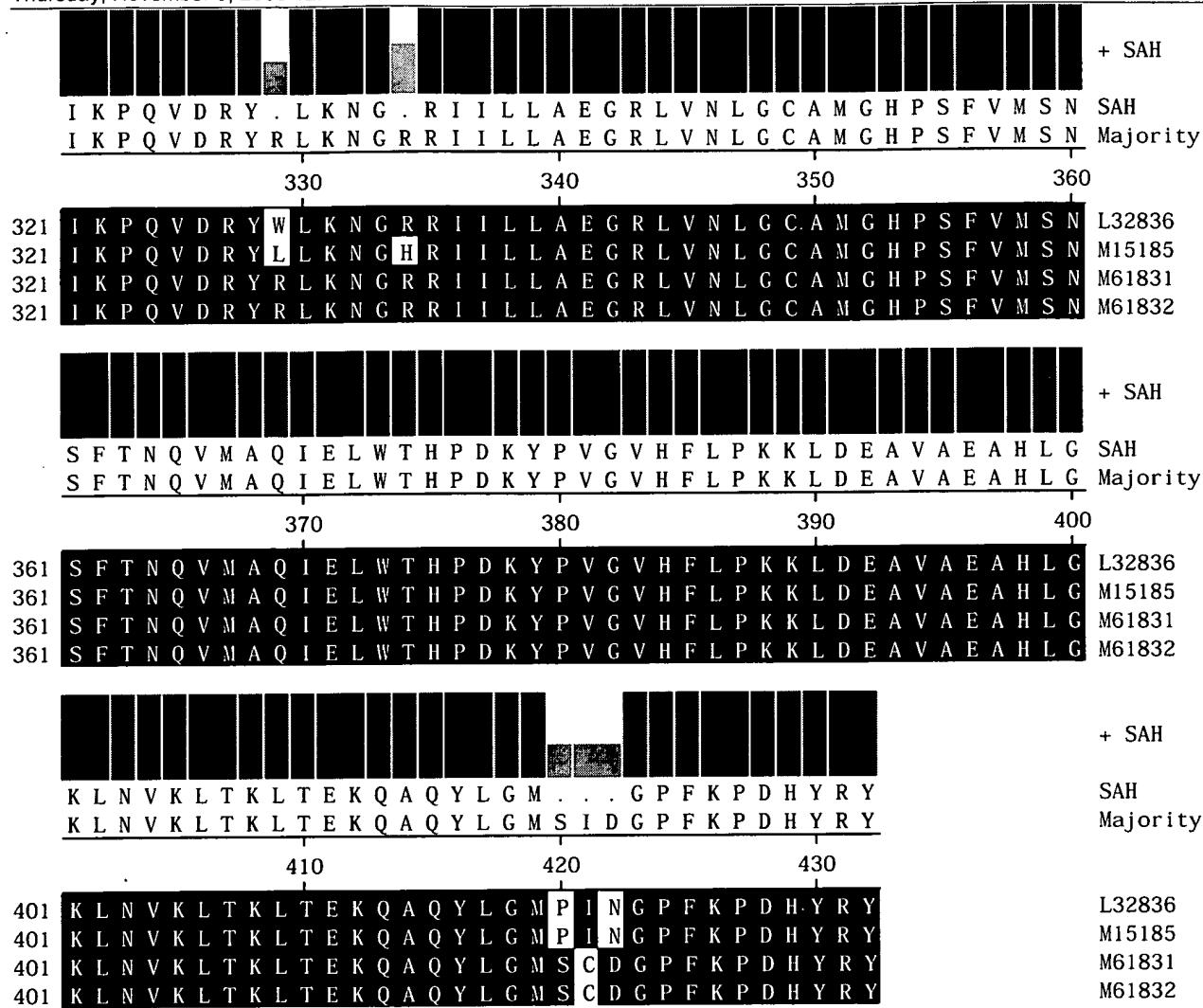
NOV 08 2005  
PAM250  
SAH  
Majority

Alignment Report of Untitled, using J. Hein method with PAM250 residue weight table.  
Thursday, November 3, 2005 12:45 PM

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Consensus 'SAH': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.